

# SEQUENCE LISTING

<110> Kretz, Keith

<120> Novel Phytase

<130> 09010/029003

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<150> 09/259,214

<151> 1999-03-01

<150> 08/910,798

<151> 1997-08-13

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

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<212> DNA

<213> Escherichia coli

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<222> (1)..(1323)

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1

5

10

15

ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt 96

Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser

20

25

30

gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg 144

Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr

35

40

45

caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta 192

Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val

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55

60

aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc tat ctc 240

Lys	Leu	Gly	Trp	Leu	Thr	Pro	Xaa	Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu	
65					70					75					80	
gga	cat	tac	caa	cgc	cag	cgt	ctg	gta	gcc	gac	gga	ttg	ctg	gcg	aaa	288
Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu	Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys	
			85						90					95		
aag	ggc	tgc	ccg	cag	tct	ggg	cag	gtc	gcg	att	att	gct	gat	gtc	gac	336
Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp	
			100					105					110			
gag	cgt	acc	cgt	aaa	aca	ggc	gaa	gcc	ttc	gcc	gcc	ggg	ctg	gca	cct	384
Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	
		115					120					125				
gac	tgt	gca	ata	acc	gta	cat	acc	cag	gca	gat	acg	tcc	agt	ccc	gat	432
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp	
		130				135					140					
ccg	tta	ttt	aat	cct	cta	aaa	act	ggc	gtt	tgc	caa	ctg	gat	aac	gcg	480
Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala	
145					150					155				160		
aac	gtg	act	gac	gcg	atc	ctc	agc	agg	gca	gga	ggg	tca	att	gct	gac	528
Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp	
				165					170				175			
ttt	acc	ggg	cat	cgg	caa	acg	gcg	ttt	cgc	gaa	ctg	gaa	cgg	gtg	ctt	576
Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu	
			180					185					190			
aat	ttt	ccg	caa	tca	aac	ttg	tgc	ctt	aaa	cgt	gag	aaa	cag	gac	gaa	624
Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu	
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Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala	
		210				215					220					
gac	aat	gtc	tca	tta	acc	ggg	gcg	gta	agc	ctc	gca	tca	atg	ctg	acg	720
Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr	
225					230					235				240		
gag	ata	ttt	ctc	ctg	caa	caa	gca	cag	gga	atg	ccg	gag	ccg	ggg	tgg	768
Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp	
			245					250						255		
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Gly	Arg	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	Leu	His	
			260					265					270			
aac	gcg	caa	ttt	tat	ttg	cta	caa	cgc	acg	cca	gag	gtt	gcc	cgc	agc	864
Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser	
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cgc	gcc	acc	ccg	tta	ttg	gat	ttg	atc	atg	gca	gcg	ttg	acg	ccc	cat	912
Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Met	Ala	Ala	Leu	Thr	Pro	His	
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cca	ccg	caa	aaa	cag	gcg	tat	ggg	gtg	aca	tta	ccc	act	tca	gta	ctg	960
Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	Val	Leu	
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ttt	att	gcc	gga	cac	gat	act	aat	ctg	gca	aat	ctc	ggc	ggc	gca	ctg	1008
Phe	Ile	Ala	Gly	His	Asp	Thr	Asn	Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu	
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gag	ctc	aac	tgg	acg	ctt	ccc	ggg	cag	ccg	gat	aac	acg	ccg	cca	ggg	1056
Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly	
		340				345				350						
ggg	gaa	ctg	gtg	ttt	gaa	cgc	tgg	cgt	cgg	cta	agc	gat	aac	agc	cag	1104
Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln	
		355				360				365						
tgg	att	cag	gtt	tcg	ctg	gtc	ttc	cag	act	tta	cag	cag	atg	cgt	gat	1152
Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp	
		370				375				380						
aaa	acg	ccg	ctg	tca	tta	aat	acg	ccg	ccc	gga	gag	gtg	aaa	ctg	acc	1200
Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr	
385				390					395					400		
ctg	gca	gga	tgt	gaa	gag	cga	aat	gcg	cag	ggc	atg	tgt	tcg	ttg	gca	1248
Leu	Ala	Gly	Cys	Glu	Glu	Arg	Asn	Ala	Gln	Gly	Met	Cys	Ser	Leu	Ala	
			405					410				415				
ggg	ttt	acg	caa	atc	gtg	aat	gaa	gca	cgc	ata	ccg	gcg	tgc	agt	ttg	1296
Gly	Phe	Thr	Gln	Ile	Val	Asn	Glu	Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu	
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Arg	Ser	His	His	His	His	His	His									
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Val	Val	Ile	Val	Ser	Arg	His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr
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Gln	Leu	Met	Gln	Asp	Val	Thr	Pro	Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val
	50					55					60				
Lys	Leu	Gly	Trp	Leu	Thr	Pro	Xaa	Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu
	65				70					75					80
Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu	Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys
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Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp
			100					105					110		
Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro
		115					120					125			
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp
	130					135					140				
Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala
145					150					155				160	
Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp
			165						170					175	
Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu
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Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu
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Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr  
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Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp  
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Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His  
 260 265 270

Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser  
 275 280 285

Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His  
 290 295 300

Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu  
 305 310 315 320

Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu  
 325 330 335

Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly  
 340 345 350

Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln  
 355 360 365

Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp  
 370 375 380

Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr  
 385 390 395 400

Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala  
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Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu  
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gtttctggat ccttacaac tgcacgccgg tat

33

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gtttctggat ccttacaac tgcacgccgg tat